

Package ‘omixVizR’

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Title A Toolkit for Omics Data Visualization

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Description Provides a suite of tools for the comprehensive visualization of multi-omics data, including genomics, transcriptomics, and proteomics. Offers user-friendly functions to generate publication-quality plots, thereby facilitating the exploration and interpretation of complex biological datasets. Supports seamless integration with popular R visualization frameworks and is well-suited for both exploratory data analysis and the presentation of final results. Key formats and methods are presented in Huang, S., et al. (2024) ``The Born in Guangzhou Cohort Study enables generational genetic discoveries" <doi:10.1038/s41586-023-06988-4>.

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URL <https://github.com/Leslie-Lu/omixVizR>

BugReports <https://github.com/Leslie-Lu/omixVizR/issues>

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MR_2SLS	<i>MR_2SLS</i>
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Description

Perform Two-Stage Least Squares (2SLS) Mendelian Randomization analysis.

Usage

```
MR_2SLS(  
  infile,  
  outcome,  
  outcome_name,  
  prs_cols_match,  
  regexr_pattern,  
  standardise = TRUE,  
  digits = 3,  
  .progress = TRUE  
)
```

Arguments

<code>infile</code>	The input file containing the data.
<code>outcome</code>	The outcome variable.
<code>outcome_name</code>	The name of the outcome variable.
<code>prs_cols_match</code>	The columns to match for PRS.
<code>regexr_pattern</code>	The regular expression pattern to use for matching.
<code>standardise</code>	Whether to standardise the prs data, Default: TRUE
<code>digits</code>	The number of decimal places to round to, Default: 3
<code>.progress</code>	Whether to show progress, Default: TRUE

Details

This function performs a Two-Stage Least Squares (2SLS) Mendelian Randomization analysis.

Value

A list containing the results of the 2SLS analysis.

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See Also

[fread](#), [as.data.table](#), [setattr](#), [setDT](#), [select](#), [reexports](#) [map](#) [str_extract](#) [nearPD](#) [cov](#) [shrink](#)

plot_forest

plot_forest

Description

Creates a forest plot overlaid on a table.

Usage

```
plot_forest(  
  p_left_data,  
  point_estimate,  
  ci_lower_bound,  
  ci_upper_bound,  
  ci_sep = ", ",  
  p_right_data = NULL,  
  precision_digits = 3,  
  p_mid_width = 30,  
  null_line_at = 1,  
  output_path = NULL,  
  dpi = 600,  
  display = TRUE,  
  font_family = c("MetroSans", "mono"),  
  p_left_data_name = NULL,  
  p_right_data_name = "Effect size (95% CI)",  
  stripe_colour = "#eff3f2",  
  background_colour = "white",  
  x_scale_linear = TRUE,  
  xlim = NULL,  
  xbreaks = NULL,  
  nudge_y = 0,  
  nudge_x = 1,  
  nudge_height = 0,  
  nudge_width = 0,  
)
```

```

justify = 0,
arrows = FALSE,
arrow_labels = c("Lower", "Higher"),
risk_colors = (ggsci::pal_npg("nrc"))(2),
arrow_nudge_y = 0,
add_plot = NULL,
add_plot_width = 1,
add_plot_gap = FALSE,
point_sizes = 3,
point_shapes = 16,
p_mid_forest = NULL,
lower_header_row = FALSE,
render_as = "png",
table_theme = NULL
)

```

Arguments

p_left_data Data frame (required). The information to be displayed to the left of the forest plot.

point_estimate Vector. The point estimates to be displayed in the forest plot.

ci_lower_bound Vector. The lower confidence bounds.

ci_upper_bound Vector. The upper confidence bounds.

ci_sep String. What should separate the low and high confidence bounds? Default " to ".

p_right_data Data frame (optional). Information to be displayed on the right side of the table. If not supplied, an Estimate column is generated automatically.

precision_digits Integer. The number of decimal places on the point_estimate (default 3)

p_mid_width Integer. The width of forest plot in characters (default 30)

null_line_at Numeric. Default 1. Change to 0 if using absolute measures.

output_path String. Where to save the image, default tempdir().

dpi Numeric. The image resolution in dpi, default 600

display Logical. Should the file be opened? Default TRUE.

font_family String or character vector. The font to use for the ggplot and table. Default c("MetroSans", "mono"). The first available font is used.

p_left_data_name String or String Vector. The name vector for the left side data. Default NULL, which uses the column names of p_left_data.

p_right_data_name String. The name vector for the right side data. Default "Effect size (95% CI)"

stripe_colour Hex String. Colour to use for the table stripes, default "#eff3f2".

background_colour Hex String or Colour Name. The colour of the background, default "white".

x_scale_linear	Logical. Default TRUE, change to FALSE for a log scale.
xlim	Vector. Manually specify limits for the x axis as a vector length 2, i.e. c(low, high)
xbreaks	Vector. X axis breaks to label. Specify limits in xlim if using this option.
nudge_y	Numeric. Allows small changes to the vertical alignment of the forest plot points. 1 unit is approximately the height of 1 row.
nudge_x	Numeric. Nudge the alignment horizontally. Default 1. Higher values make the entire plot wider and consequently space out the elements of the figure.
nudge_height	Numeric. Adjust the overall height of the plot output. Default is 0.
nudge_width	Numeric. Adjust the overall width of the plot output. Default is 0.
justify	Numeric Vector. This should be a numeric vector either of length 1 (in which case it will apply to all columns) or of length equal to the number of columns in p_left_data + 1 (for the point_estimate column). Each number in the vector dictates the column justification, with 0 being left, 0.5 being center, and 1 being right.
arrows	Logical. Should there be arrows displayed below the ggplot? Default FALSE. Specify xlim if using arrows.
arrow_labels	String Vector, length 2. Labels for the arrows. Set arrows to TRUE or this will have no effect.
risk_colors	Vector. Length 2. Colors for the effect measure. Default is ggsci::pal_npg("nrc")(2).
arrow_nudge_y	Numeric. Nudge the vertical position of the arrows. Default 0.
add_plot	A ggplot object to add to the right side of the table. To align correctly with rows, 1 unit is the height of a row and y = 0 for the center of the bottom row.
add_plot_width	Numeric. Width to display add_plot. Relative to the width of the forest plot, where 1 (the default) is the same width.
add_plot_gap	Logical. Should there be space added between the plot and the main figure? Default FALSE.
point_sizes	Vector. Length should be equal to 1 or nrow(p_left_data). The sizes of the points in the center plot, where 3.25 is the default.
point_shapes	Vector. Length should be equal to 1 or nrow(p_left_data). The shapes of the points in the center plot, where 16 (a filled circle) is the default.
p_mid_forest	A ggplot object to use instead of the central plot.
lower_header_row	Logical. If TRUE, drops the header down one row (In the table rather than above it, like the default value (FALSE))
render_as	String or Function. What output format should be used? Option is passed to ggplot2::ggsave() as the argument "device". Either pass a device function (e.g. png) or one of "eps", "ps", "tex" (pictex), "pdf", "jpeg", "tiff", "png", "bmp", "svg" or "wmf" (windows only).
table_theme	A gridExtra table theme. If specified, overwrites all table theme customization in other options. The default is a modified version of ttheme_minimal.

Details

This function creates a forest plot overlaid on a table. It is highly customizable, allowing for adjustments to fonts, colors, and layout.

Value

image

Author(s)

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plot_gwas_power	<i>plot_gwas_power</i>
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Description

Generates a statistical power analysis plot for GWAS studies. Supports binary (case-control) traits over a range of odds ratios and minor allele frequencies, and quantitative traits over a range of effect sizes and minor allele frequencies. This function uses the 'genpwr' package for calculations and creates a highly customized ggplot.

Usage

```
plot_gwas_power(  
  trait_type = "bt",  
  n_cases = NULL,  
  n_controls = NULL,  
  sd_trait = NULL,  
  N = NULL,  
  maf_levels = c(0.01, 0.02, 0.05, 0.1, 0.2, 0.5),  
  or_range = seq(1.01, 2, 0.001),  
  effect_size = seq(0.01, 0.3, 0.001),  
  alpha = 5e-08,  
  plot_title = NULL,  
  save_plot = TRUE,  
  output_graphics = "png",  
  width = 17,  
  height = 9,  
  dpi = 600  
)
```

Arguments

trait_type	Character string specifying trait type: "bt" for binary (case-control) or "qt" for quantitative traits. Default: "bt".
n_cases	Number of cases in the study (required if trait_type = "bt").

n_controls	Number of controls in the study (required if trait_type = "bt").
sd_trait	Numeric, standard deviation of the quantitative trait (required if trait_type = "qt").
N	Numeric, total sample size for quantitative traits (required if trait_type = "qt").
maf_levels	A numeric vector of Minor Allele Frequencies (MAFs) to test. Default: c(0.01, 0.02, 0.05, 0.10, 0.20, 0.50).
or_range	A numeric vector specifying the sequence of Odds Ratios (ORs) to test. Default: seq(1.01, 2.00, 0.001). Used when trait_type = "bt".
effect_size	A numeric vector specifying the sequence of effect sizes (beta) to test for quantitative traits. Default: seq(0.01, 0.30, 0.001). Used when trait_type = "qt".
alpha	The significance level (alpha) for the power calculation. Default: 5e-8.
plot_title	A string for the plot title. Default: Cases / Controls for binary traits or Sample Size for quantitative traits.
save_plot	Logical, whether to save the plot to a file. If FALSE, the plot object is only returned. Default: TRUE.
output_graphics	The file format for saving the plot. Currently supports "png" and "pdf". Default: "png".
width	The width of the saved plot in inches. Default: 17.
height	The height of the saved plot in inches. Default: 9.
dpi	The resolution of the saved plot in dots per inch. Default: 600.

Details

This function automates the process of calculating and visualizing GWAS power for both binary (case-control) and quantitative traits. For binary traits, it analyzes power across odds ratios, while for quantitative traits, it analyzes power across effect sizes. It highlights the minimum OR/effect size required to achieve 80% power for the lowest and third-lowest MAF levels, adding dashed lines and color-coded labels for clarity.

Value

A list containing two elements:

plot	The ggplot object for the power plot.
power_data	A data.table containing the full results from the power analysis.

Font Information

The MetroSans font included in this package is intended for academic research and non-commercial use only. For commercial use, please contact the font copyright holder.

The font files are included in the package's inst/extdata directory and are automatically loaded for plotting.

Author(s)

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Examples

```
# Binary trait example (case-control)
power_results_bt <- plot_gwas_power(
  trait_type = "bt",
  n_cases = 4324,
  n_controls = 93945,
  save_plot = FALSE
)

# Quantitative trait example
power_results_qt <- plot_gwas_power(
  trait_type = "qt",
  sd_trait = 0.09365788681305078,
  N = 10000,
  maf_levels = c(0.01, 0.02, 0.05, 0.10, 0.20, 0.50),
  effect_size = seq(0.01, 0.10, 0.001),
  save_plot = FALSE
)

# Access the ggplot object and data
# print(power_results_bt$plot)
# print(power_results_bt$power_data)
```

plot_heatmap

plot_heatmap

Description

Generate a heatmap for a given correlation matrix.

Usage

```
plot_heatmap(
  cor_mat,
  scale = "none",
  show_rownames = FALSE,
  show_colnames = FALSE,
  labels_row = NULL,
  labels_col = NULL,
  breaks = seq(-1, 1, length.out = 101),
  legend_breaks = c(-1, -0.5, 0, 0.5, 1),
  legend_labels = c("-1.0", "-0.5", "0", "0.5", "1.0"),
  legend_name = "Correlation",
```

```
    output_path = NULL,  
    display = TRUE,  
    render_as = "png",  
    width = 18,  
    height = 16,  
    dpi = 600  
  )
```

Arguments

cor_mat	A numeric matrix representing the correlation values.
scale	Character string indicating how to scale the data. Default is 'none'.
show_rownames	Logical indicating whether to show row names. Default is FALSE.
show_colnames	Logical indicating whether to show column names. Default is FALSE.
labels_row	Character vector of labels for the rows. Default is NULL.
labels_col	Character vector of labels for the columns. Default is NULL.
breaks	Numeric vector of breakpoints for the heatmap colors. Default is seq(-1, 1, length.out = 101).
legend_breaks	Numeric vector of breakpoints for the legend. Default is c(-1, -0.5, 0, 0.5, 1).
legend_labels	Character vector of labels for the legend. Default is c("-1.0", "-0.5", "0", "0.5", "1.0").
legend_name	Character string for the legend title. Default is 'Correlation'.
output_path	Character string for the output file path. Default is NULL.
display	Logical indicating whether to display the plot. Default is TRUE.
render_as	Character string indicating the file format to save the plot. Default is 'png'.
width	Numeric indicating the width of the plot. Default is 18.
height	Numeric indicating the height of the plot. Default is 16.
dpi	Numeric indicating the resolution of the plot. Default is 600.

Details

This function generates a heatmap for a given correlation matrix.

Value

A heatmap plot.

Author(s)

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plot_qqman	<i>plot_qqman</i>
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Description

Create GWAS QQ & Manhattan Plots.

Usage

```
plot_qqman(
  plink_assoc_file,
  pheno_name,
  maf_filter = NULL,
  gwas_threshold = 5e-08,
  label_col = "SNP",
  output_graphics = "png",
  save_plot = TRUE,
  lambda1_qq_pos = c(2.1, -5.5),
  lambda2_qq_pos = c(1.565, -4)
)
```

Arguments

plink_assoc_file	Path to the PLINK association file.
pheno_name	Phenotype name.
maf_filter	Minor allele frequency filter, Default: NULL
gwas_threshold	The significance threshold for highlighting SNPs. Default: 5e-8.
label_col	The name of the column to use for labeling significant SNPs. Default: "SNP".
output_graphics	Output graphics format, Default: 'png'
save_plot	Logical, whether to save plots to files. If FALSE, plots are only displayed. Default: TRUE
lambda1_qq_pos	A numeric vector of length 2 specifying the c(hjust, vjust) for the lambda text in the QQ plot. Default: c(2.1, -5.5).
lambda2_qq_pos	A numeric vector of length 2 specifying the c(hjust, vjust) for the SNP count (N) text in the QQ plot. Default: c(1.565, -4.0).

Details

This function reads a PLINK association file and generates Manhattan and QQ plots for the GWAS results.

Value

A list containing the ggplot objects for the Manhattan and QQ plots.

Font Information

The MetroSans font included in this package is intended for academic research and non-commercial use only. For commercial use, please contact the font copyright holder.

The font files are included in the package's inst/extdata directory and are automatically loaded for plotting.

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Examples

```
sample_file <- system.file("extdata", "sample_gwas.assoc.linear", package = "omixVizR")

# Check if the file exists before running the example
if (file.exists(sample_file)) {
  # Run the function with the sample data
  plots <- plot_qqman(
    plink_assoc_file = sample_file,
    pheno_name = "SamplePheno",
    save_plot = FALSE
  )
  # You can then access the plots like this:
  # print(plots$manhattan_plot)
  # print(plots$qq_plot)
} else {
  message("Sample file not found, skipping example.")
}
```

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